

Figure 1

MKEIAMRNSKRKPEPTFAGKKLRSTRLLRRKRAQISPVLVQSPLMWSKQIGVSAASVDSCS 60
 DLIADDNVSCGSSRVEKSSNPKKTLIEEVEVSKPGYNVKETIGDSKFRRI TRSYSKLHKE 120
 KEGDEIEVSESSCVDNSGAGLRRLLNVKGNKINDNDIEISFRSDVTFAGHVSNSRSLNFE 180
 SENKESDVVSVTSGVEYCSKFGSVTGGADNEEIEISKPSFVEADSSILGSAKELKPELEI 240
 VGCVSDLACSEKFSSEEVSDSLDDSESEQRSEIYSQYSDFDYDYPISIFFDSGSEFSEKS 300
 SSDSPI SHRSIYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDDEVEEESYLRRLERE 360
 RSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETIFLGVGLLDRFLS 420
 KGSFKSERTLLVGLIASLTATRIEENQPYNSIRKRNFTIQNLYSRHEVVAMEWLVQEV 480
 LNFKCFPTTIFNFWFLYIKARANPEVERKASLAVTSLSDQTQLCFWPSTVAAALVVLAV 540
 CIEHNKISAYQRVIKVHVRTTDNELPECVKSIDWLLGQ 578

Figure 2

SDS	377	MDN-TGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSF	424
cyc2b		MAQQFDISDKMRAILIDWLIIEVHDKFELMNETLFLTIVNLIDRFLSKQAV	
cyc2a		M-QQIDINEKMRAILIDWLIIEVHDKFELMNETLFLTIVNLIDRFLSKQNV	
Consensus		M + ++R+I++ W++ L +ETLFL+V L+DRFLSK	
SDS	425	KSERTLILVGIASLTATRIEE-NQPYNSIRKRNFTIQNLYSRHEVVA	472
cyc2b		-ARKKLQVLVGLVALLLACKYEEVSP---IVEDLVVISDKAYTRTDVLE	
cyc2a		-MRKKLQVLVGLVALLLACKYEEVSP---VVEDLVVISDKAYTRNDVLE	
Consensus		+ L LVG+ +L LA + EE P + I Y+R +V+	
SDS	473	MEWLIVQEVINFKCFTPTIFNFLWFLKAAARANPEVERKAKSLAVTSLSD	521
cyc2b		MEKIMLSTLQFNMSLPTQYPFLKRFLKAAQSDKKLEILASFLIELALVD	
cyc2a		MEKTMSTLQFNISLPTQYPFLKRFLKAAQADKKCEVLASFLIELALVE	
Consensus		ME - L+F PT + FL +LKAA A E A L +L D	

Figure 3

	SDS	cyc2b	cyc2a	cyc3b	cycD
SDS	100%	34%/52%	34%/52%	28%/49%	21%/42%
cyc2b		100%	87%/92%	40%/60%	21%/43%
cyc2a			100%	46%/64%	22%/43%
cyc3b				100%	22%/41%